Biomarker Development for Early Detection of Hepatocellular Carcinoma Using Proteomics

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Hepatocellular carcinoma (HCC) is one of the world's leading cancer-related mortalities. In Vietnam, HCC ranks second in cancer incidence and accounts for more than 25,000 deaths annually. To improve prognosis and overall survival, it is essential to identify patients with HCC at an early stage. However, current screening methods, including imaging and blood tests, have limited sensitivity and specificity for detecting early-stage tumors. Although several studies have identified potential protein biomarkers in the blood across different populations, these have not been investigated in Vietnam. In this study, we examined alterations in the plasma proteome between control subjects and patients with HCC in Vietnamese individuals. Using LC–MS-based proteomic analysis, we identified a total of 474 proteins, with an average of 394 proteins detected across 30 participants. Principal component analysis revealed a clear separation between the HCC group and the other groups, indicating distinct plasma proteomic profiles. To identify potential biomarkers for HCC, ANOVA followed by Tukey's Honest Significant Difference was performed, revealing 38 differentially expressed proteins (DEPs), including 10 cancer-specific upregulated and 22 cancer-specific downregulated proteins. These DEPs were further used for gene set enrichment analysis and showed associations with biological processes involved in HCC progression, such as lipid metabolism, coagulation, and the inflammatory response. Together, these analyses provide a foundation for developing a multi-protein biomarker panel for the early diagnosis of HCC in the Vietnamese population.

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